

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: November 7, 2006, 18:11:36 ; Search time 202 Seconds  
(without alignments)  
1892.242 Million cell updates/sec

Title: US-10-781-564-1  
Perfect score: 4392  
Sequence: 1 MAGLNCGVSIALLGVLLGA.....SSKDTDIPLLSTQEPMEPAE 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	4392	100.0		836	8	ADR47303	Adr47303 Human SIM
2	4392	100.0		836	9	AEA01805	Aea01805 Human CUB
3	4392	100.0		836	10	AEE80622	Aee80622 Human ova
4	4385	99.8		836	5	ABP69553	Abp69553 Human pol
5	4385	99.8		836	5	AAM49641	Aam49641 Human tum
6	4385	99.8		836	10	AEE80621	Aee80621 Human ova
7	4059	92.4		770	10	AEE79913	Aee79913 Human ova
8	3638.5	82.8		709	3	AAY91456	Aay91456 Human sec
9	3638.5	82.8		709	8	ADL71528	Adl71528 Novel hum
10	3463	78.8		749	5	AAM49640	Aam49640 Human tum
11	3410	77.6		649	4	AAB95558	Aab95558 Human pro
12	3410	77.6		649	10	AEE80623	Aee80623 Human ova
13	2168	49.4		487	10	AEE79914	Aee79914 Human ova
14	2155	49.1		414	8	ADL71669	Adl71669 Novel hum
15	2155	49.1		443	3	AAY91592	Aay91592 Human sec
16	2155	49.1		443	8	ADL71667	Adl71667 Novel hum

17	1779	40.5	343	4	AAU12252	Aau12252	Human	PRO
18	1779	40.5	343	6	ABO17696	Abo17696	Novel	hum
19	1779	40.5	343	6	ABU80950	Abu80950	Human	PRO
20	1779	40.5	343	6	ABU66650	Abu66650	Human	PRO
21	1779	40.5	343	6	ABU59731	Abu59731	Novel	sec
22	1779	40.5	343	6	ABO24921	Abo24921	Human	sec
23	1779	40.5	343	6	ABU66926	Abu66926	Human	sec
24	1779	40.5	343	6	ADA45681	Ada45681	Novel	hum
25	1779	40.5	343	6	ADA76112	Ada76112	Human	PRO
26	1779	40.5	343	6	ADA18762	Ada18762	Human	PRO
27	1779	40.5	343	6	ADA61385	Ada61385	Homo sapi	
28	1779	40.5	343	6	ADB19170	Adb19170	Novel	hum
29	1779	40.5	343	6	ADB27711	Adb27711	Human	PRO
30	1779	40.5	343	6	ADA86190	Ada86190	Novel	hum
31	1779	40.5	343	6	ADB15754	Adb15754	Human	PRO
32	1779	40.5	343	6	ADA47540	Ada47540	Human	PRO
33	1779	40.5	343	6	ADA67335	Ada67335	Human	PRO
34	1779	40.5	343	6	ADB30342	Adb30342	Human	PRO
35	1779	40.5	343	6	ADA85638	Ada85638	Novel	hum
36	1779	40.5	343	6	ADA96850	Ada96850	Human	PRO
37	1779	40.5	343	6	ADA79154	Ada79154	Human	PRO
38	1779	40.5	343	6	ADA87293	Ada87293	Novel	hum
39	1779	40.5	343	6	ADB16495	Adb16495	Human	PRO
40	1779	40.5	343	6	ADA91587	Ada91587	Novel	hum
41	1779	40.5	343	6	ADB14650	Adb14650	Human	PRO
42	1779	40.5	343	6	ADB18611	Adb18611	Novel	hum
43	1779	40.5	343	6	ADA93826	Ada93826	Human	PRO
44	1779	40.5	343	6	ADB19722	Adb19722	Novel	hum
45	1779	40.5	343	6	ADB13034	Adb13034	Human	PRO

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OM protein - protein search, using sw model

Run on: November 7, 2006, 18:21:46 ; Search time 54 Seconds  
(without alignments)  
1355.104 Million cell updates/sec

Title: US-10-781-564-1  
Perfect score: 4392  
Sequence: 1 MAGLNCGVSIALLGVLLGA.....SSKDTDIPLLSTQEPMEPAE 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : Issued Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3638.5	82.8	709	2	US-09-489-847-132	Sequence 132, App
2	2155	49.1	414	2	US-09-489-847-273	Sequence 273, App
3	2155	49.1	443	2	US-09-489-847-271	Sequence 271, App
4	827	18.8	159	2	US-09-489-847-272	Sequence 272, App
5	141	3.2	3623	2	US-09-341-461-2	Sequence 2, Appli
6	126.5	2.9	590	2	US-09-902-540-11386	Sequence 11386, A
7	117.5	2.7	2476	1	US-08-276-967-2	Sequence 2, Appli
8	117	2.7	2766	2	US-09-964-956-62	Sequence 62, Appl
9	114.5	2.6	771	2	US-09-854-845-47	Sequence 47, Appl
10	114.5	2.6	870	2	US-09-854-845-31	Sequence 31, Appl
11	114	2.6	766	2	US-09-854-845-49	Sequence 49, Appl
12	114	2.6	865	2	US-09-854-845-33	Sequence 33, Appl
13	114	2.6	1589	2	US-08-755-587-189	Sequence 189, App
14	113.5	2.6	1518	2	US-10-142-650-2	Sequence 2, Appli
15	113.5	2.6	1719	1	US-08-459-568-4	Sequence 4, Appli
16	113.5	2.6	1719	1	US-08-399-411-4	Sequence 4, Appli
17	113.5	2.6	1719	2	US-08-516-859A-4	Sequence 4, Appli
18	113.5	2.6	1719	2	US-09-586-472-4	Sequence 4, Appli
19	113.5	2.6	1719	2	US-09-528-706-4	Sequence 4, Appli

20	113.5	2.6	1719	2	US-10-024-450-4	Sequence 4, Appli
21	113.5	2.6	1719	2	US-10-142-650-1	Sequence 1, Appli
22	112.5	2.6	690	2	US-09-248-796A-19169	Sequence 19169, A
23	112.5	2.6	744	2	US-09-854-845-43	Sequence 43, Appl
24	112.5	2.6	843	2	US-09-854-845-27	Sequence 27, Appl
25	112	2.6	739	2	US-09-854-845-45	Sequence 45, Appl
26	112	2.6	838	2	US-09-854-845-29	Sequence 29, Appl
27	112	2.6	1540	2	US-09-949-016-11382	Sequence 11382, A
28	112	2.6	1540	2	US-09-949-016-11383	Sequence 11383, A
29	111.5	2.5	440	2	US-09-538-092-999	Sequence 999, App
30	111.5	2.5	451	2	US-09-949-016-9282	Sequence 9282, Ap
31	110.5	2.5	1694	2	US-09-560-385A-12	Sequence 12, Appl
32	110.5	2.5	1725	2	US-09-560-385A-10	Sequence 10, Appl
33	109	2.5	699	2	US-09-949-016-6138	Sequence 6138, Ap
34	107.5	2.4	649	2	US-09-248-796A-20641	Sequence 20641, A
35	107.5	2.4	679	2	US-09-874-198-6	Sequence 6, Appli
36	106.5	2.4	683	2	US-09-213-293D-1	Sequence 1, Appli
37	106.5	2.4	866	2	US-09-527-084A-4	Sequence 4, Appli
38	106.5	2.4	2343	2	US-09-324-867-2	Sequence 2, Appli
39	106	2.4	670	1	US-08-473-750-11	Sequence 11, Appl
40	106	2.4	670	1	US-08-477-326-11	Sequence 11, Appl
41	106	2.4	717	2	US-09-949-016-11182	Sequence 11182, A
42	105.5	2.4	369	2	US-09-107-532A-5754	Sequence 5754, Ap
43	104	2.4	449	1	US-08-839-008-2	Sequence 2, Appli
44	104	2.4	458	2	US-09-949-016-7238	Sequence 7238, Ap
45	104	2.4	766	2	US-10-297-895A-21	Sequence 21, Appl

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OM protein - protein search, using sw model

Run on: November 7, 2006, 18:33:56 ; Search time 190 Seconds  
(without alignments)  
2038.145 Million cell updates/sec

Title: US-10-781-564-1  
Perfect score: 4392  
Sequence: 1 MAGLNCGVSIALLGVLLGA.....SSKDTDIPLLSTQEPMEPAE 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : Published\_Applications\_AA Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4392	100.0	836	5	US-10-781-564-1
2	4392	100.0	836	6	US-11-050-857-989
3	4385	99.8	836	3	US-09-899-569A-4
4	4385	99.8	836	6	US-11-050-857-988
5	4059	92.4	770	6	US-11-050-857-252
6	3638.5	82.8	709	4	US-10-351-334-132
7	3638.5	82.8	709	6	US-11-229-769-132
8	3463	78.8	749	3	US-09-899-569A-2
9	3410	77.6	649	6	US-11-050-857-990
10	2608	59.4	495	6	US-11-050-857-1135
11	2168	49.4	487	6	US-11-050-857-253
12	2155	49.1	414	4	US-10-351-334-273
13	2155	49.1	414	6	US-11-229-769-273
14	2155	49.1	443	4	US-10-351-334-271
15	2155	49.1	443	6	US-11-229-769-271
16	1779	40.5	343	4	US-10-028-072-162
17	1779	40.5	343	4	US-10-140-808-162
18	1779	40.5	343	4	US-10-121-049-162
19	1779	40.5	343	4	US-10-123-904-162
20	1779	40.5	343	4	US-10-140-470-162

21	1779	40.5	343	4	US-10-175-746-162	Sequence 162, App
22	1779	40.5	343	4	US-10-176-918-162	Sequence 162, App
23	1779	40.5	343	4	US-10-176-921-162	Sequence 162, App
24	1779	40.5	343	4	US-10-137-865-162	Sequence 162, App
25	1779	40.5	343	4	US-10-140-474-162	Sequence 162, App
26	1779	40.5	343	4	US-10-142-431-162	Sequence 162, App
27	1779	40.5	343	4	US-10-143-114-162	Sequence 162, App
28	1779	40.5	343	4	US-10-142-419-162	Sequence 162, App
29	1779	40.5	343	4	US-10-123-262-162	Sequence 162, App
30	1779	40.5	343	4	US-10-142-423-162	Sequence 162, App
31	1779	40.5	343	4	US-10-121-050-162	Sequence 162, App
32	1779	40.5	343	4	US-10-141-755-162	Sequence 162, App
33	1779	40.5	343	4	US-10-143-032-162	Sequence 162, App
34	1779	40.5	343	4	US-10-123-108-162	Sequence 162, App
35	1779	40.5	343	4	US-10-123-236-162	Sequence 162, App
36	1779	40.5	343	4	US-10-123-261-162	Sequence 162, App
37	1779	40.5	343	4	US-10-140-921-162	Sequence 162, App
38	1779	40.5	343	4	US-10-140-928-162	Sequence 162, App
39	1779	40.5	343	4	US-10-121-045-162	Sequence 162, App
40	1779	40.5	343	4	US-10-123-292-162	Sequence 162, App
41	1779	40.5	343	4	US-10-123-903-162	Sequence 162, App
42	1779	40.5	343	4	US-10-124-819-162	Sequence 162, App
43	1779	40.5	343	4	US-10-124-822-162	Sequence 162, App
44	1779	40.5	343	4	US-10-140-925-162	Sequence 162, App
45	1779	40.5	343	4	US-10-160-498-162	Sequence 162, App

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OM protein - protein search, using sw model

Run on: November 7, 2006, 18:35:16 ; Search time 45 Seconds  
(without alignments)  
1555.808 Million cell updates/sec

Title: US-10-781-564-1  
Perfect score: 4392  
Sequence: 1 MAGLNCGVSIALLGVLLLG.....SSKDTDIPLLSTQEPMEPAE 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 320231 seqs, 83745634 residues

Total number of hits satisfying chosen parameters: 320231

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	138	3.1	4051	6	US-10-501-834-7	Sequence 7, Appli
2	122.5	2.8	3387	6	US-10-669-920-448	Sequence 448, App
3	122.5	2.8	4059	6	US-10-501-834-6	Sequence 6, Appli
4	118	2.7	3609	6	US-10-669-920-451	Sequence 451, App
5	117	2.7	1045	7	US-11-056-355B-73120	Sequence 73120, A
6	112	2.6	273	7	US-11-174-307B-3974	Sequence 3974, Ap
7	111.5	2.5	1263	7	US-11-330-403-13062	Sequence 13062, A
8	110.5	2.5	942	7	US-11-056-355B-106452	Sequence 106452,
9	110.5	2.5	942	7	US-11-056-355B-117691	Sequence 117691,
10	109	2.5	911	7	US-11-056-355B-106453	Sequence 106453,
11	109	2.5	911	7	US-11-056-355B-117692	Sequence 117692,
12	107.5	2.4	728	6	US-10-527-191-13	Sequence 13, Appl
13	107	2.4	811	6	US-10-374-780A-278	Sequence 278, App
14	106.5	2.4	800	6	US-10-953-349-33871	Sequence 33871, A
15	106.5	2.4	809	6	US-10-953-349-33870	Sequence 33870, A
16	106.5	2.4	867	6	US-10-953-349-33869	Sequence 33869, A
17	106.5	2.4	905	6	US-10-612-783-5587	Sequence 5587, Ap
18	106.5	2.4	1490	7	US-11-377-316-171	Sequence 171, App

19	106	2.4	699	6	US-10-527-191-14	Sequence 14, Appl
20	106	2.4	750	7	US-11-056-355B-73248	Sequence 73248, A
21	106	2.4	885	7	US-11-056-355B-73247	Sequence 73247, A
22	106	2.4	911	7	US-11-056-355B-73246	Sequence 73246, A
23	106	2.4	2412	6	US-10-527-191-70	Sequence 70, Appl
24	106	2.4	2412	6	US-10-527-191-105	Sequence 105, App
25	105.5	2.4	1272	7	US-11-330-403-14265	Sequence 14265, A
26	105.5	2.4	4590	6	US-10-505-928-569	Sequence 569, App
27	104.5	2.4	846	7	US-11-056-355B-73122	Sequence 73122, A
28	104.5	2.4	873	7	US-11-056-355B-73121	Sequence 73121, A
29	104	2.4	732	7	US-11-353-451-6	Sequence 6, Appli
30	104	2.4	2260	7	US-11-375-359-90	Sequence 90, Appl
31	104	2.4	2260	7	US-11-073-360-160	Sequence 160, App
32	104	2.4	2347	7	US-11-365-989-202	Sequence 202, App
33	104	2.4	2347	7	US-11-375-359-89	Sequence 89, Appl
34	104	2.4	2347	7	US-11-073-360-161	Sequence 161, App
35	103.5	2.4	603	7	US-11-330-403-2559	Sequence 2559, Ap
36	103	2.3	1738	7	US-11-365-989-54	Sequence 54, Appl
37	102	2.3	1614	7	US-11-056-355B-88827	Sequence 88827, A
38	102	2.3	1614	7	US-11-056-355B-92583	Sequence 92583, A
39	102	2.3	1660	7	US-11-056-355B-88826	Sequence 88826, A
40	102	2.3	1660	7	US-11-056-355B-92582	Sequence 92582, A
41	102	2.3	1828	7	US-11-056-355B-88825	Sequence 88825, A
42	102	2.3	1828	7	US-11-056-355B-92581	Sequence 92581, A
43	102	2.3	1842	7	US-11-056-355B-82005	Sequence 82005, A
44	102	2.3	1850	7	US-11-056-355B-82004	Sequence 82004, A
45	102	2.3	1895	7	US-11-056-355B-82003	Sequence 82003, A



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OM protein - protein search, using sw model

Run on: November 7, 2006, 18:16:21 ; Search time 47 Seconds  
(without alignments)  
1711.430 Million cell updates/sec

Title: US-10-781-564-1  
Perfect score: 4392  
Sequence: 1 MAGLNCGVSIALLGVLLLGA.....SSKDTDIPLLSTQEPMEPAE 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	137.5	3.1	3623	2	T08618	intrinsic factor-B
2	121.5	2.8	986	2	T33135	hypothetical prote
3	118	2.7	3623	2	T09456	intrinsic factor-B
4	117.5	2.7	1464	2	S58984	development protei
5	117.5	2.7	2476	2	T34022	zonadhesin - pig
6	116	2.6	2499	1	A30788	mannose 6-phosphat
7	115	2.6	1228	2	S46754	hypothetical prote
8	114	2.6	1224	2	T40765	web1 protein homol
9	113.5	2.6	1721	1	I38902	retinoblastoma bin
10	113	2.6	582	1	VCVDAR	env polyprotein -
11	113	2.6	603	2	T24315	hypothetical prote
12	112.5	2.6	1027	2	T19173	hypothetical prote
13	112.5	2.6	1185	2	T19212	hypothetical prote
14	111.5	2.5	440	2	A39613	oligodendrocyte-my
15	111.5	2.5	1263	2	AH2011	heterocyst glycoli
16	111	2.5	1694	2	S50065	sialoadhesin - mou
17	111	2.5	3329	2	T42205	breast cancer susc
18	111	2.5	3329	2	T30904	breast cancer tumo
19	110.5	2.5	818	2	S57078	probable protein k
20	110.5	2.5	942	1	JQ1674	protein kinase TMK
21	110	2.5	5762	2	A41819	proline-rich pepti
22	109.5	2.5	692	1	S59833	DNA-directed DNA p

23	109.5	2.5	737	2	T31349	hypothetical prote
24	109.5	2.5	4131	2	T21085	hypothetical prote
25	109	2.5	699	1	I54763	Ra-reactive factor
26	109	2.5	1091	1	IJCHNL	neural cell adhesi
27	108.5	2.5	1828	2	A40115	microtubule-associ
28	107	2.4	4919	2	T31105	hypothetical prote
29	106.5	2.4	866	2	T01171	G1/S transition co
30	106.5	2.4	1487	2	S15904	alpha-1 proteinase
31	106	2.4	737	2	T16737	hypothetical prote
32	106	2.4	830	2	T37973	rad16 nucleotide e
33	106	2.4	2180	2	A47651	zinc-finger protei
34	105.5	2.4	2083	2	T42721	CRP-ductin-alpha p
35	104.5	2.4	6805	2	S20901	titin - rabbit (fr
36	104.5	2.4	26926	1	I38344	titin, cardiac mus
37	104	2.4	1495	2	T31434	densin-180 - rat
38	104	2.4	1565	2	AD2135	polyketide synthas
39	104	2.4	2347	1	TVHURS	kinase-related pro
40	103.5	2.4	558	2	T37567	probable NADPH cyt
41	103.5	2.4	727	2	G01792	transcription fact
42	103.5	2.4	810	1	A33380	interleukin-4 rece
43	103	2.3	449	2	A55362	procollagen I C-pr
44	102.5	2.3	914	2	B96592	hypothetical prote
45	102.5	2.3	1272	2	C96637	hypothetical prote

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OM protein - protein search, using sw model

Run on: November 7, 2006, 18:12:41 ; Search time 317 Seconds  
(without alignments)  
2439.473 Million cell updates/sec

Title: US-10-781-564-1  
Perfect score: 4392  
Sequence: 1 MAGLNCGVSIALLGVLLLGA.....SSKDTDIPLLSTQEPMEPAE 836

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4392	100.0	836	1 CDCP1_HUMAN	Q9h5v8 homo sapien
2	3583.5	81.6	833	1 CDCP1_MOUSE	Q5u462 mus musculu
3	836	19.0	867	2 Q4T223_TETNG	Q4t223 tetraodon n
4	832	18.9	825	2 Q4T7U3_TETNG	Q4t7u3 tetraodon n
5	616	14.0	793	2 Q58EM7_BRARE	Q58em7 brachydanio
6	141	3.2	746	2 O01654_HALRO	O01654 halocynthia
7	141	3.2	887	2 Q60NX4_CAEBR	Q60nx4 caenorhabdi
8	140.5	3.2	2796	1 CSMD3_MOUSE	Q80t79 mus musculu
9	139.5	3.2	888	2 Q51F10_ENTHI	Q51f10 entamoeba h
10	139	3.2	746	2 Q8IAD8_HALRO	Q8iad8 halocynthia
11	137.5	3.1	719	2 Q9PVY2_TRISC	Q9pvy2 triakis scy
12	137.5	3.1	3623	1 CUBN_RAT	O70244 rattus norv
13	134.5	3.1	3623	1 CUBN_MOUSE	Q9jlb4 mus musculu
14	128	2.9	1610	2 Q498K4_XENLA	Q498k4 xenopus lae
15	127.5	2.9	4060	2 Q6T3A5_MOUSE	Q6t3a5 mus musculu
16	126.5	2.9	508	2 Q18530_CAEEL	Q18530 caenorhabdi
17	126.5	2.9	1105	2 Q4D0W0_TRYCR	Q4d0w0 trypanosoma
18	126	2.9	3670	1 CSMD3_HUMAN	Q7z407 homo sapien
19	125.5	2.9	1634	1 LR37A_HUMAN	O60309 homo sapien
20	125	2.8	595	1 SIG12_HUMAN	Q96pql homo sapien
21	123.5	2.8	1380	2 Q8NE38_HUMAN	Q8ne38 homo sapien
22	123.5	2.8	3620	1 CUBN_CANFA	Q9tu53 canis famil
23	122.5	2.8	421	2 Q7YYC4_CRYPV	Q7yyc4 cryptospori
24	122.5	2.8	1382	2 Q5JYP0_HUMAN	Q5jyp0 homo sapien

25	122.5	2.8	1406	2	Q9Y2I6_HUMAN	Q9y2i6	homo sapien
26	122.5	2.8	4059	2	Q8CIS7_MOUSE	Q8cis7	mus musculu
27	122	2.8	944	2	Q6CSE5_KLULA	Q6cse5	kluyveromyc
28	121.5	2.8	2302	2	Q5F4U0_CAEEL	Q5f4u0	caenorhabdi
29	121	2.8	766	2	Q618F0_CAEBR	Q618f0	caenorhabdi
30	121	2.8	3158	2	Q4TAD4_TETNG	Q4tad4	tetraodon n
31	120.5	2.7	708	2	Q2VPN1_XENLA	Q2vpn1	xenopus lae
32	120.5	2.7	3121	2	O42269_BRARE	O42269	brachydanio
33	120.5	2.7	3570	2	Q7Q737_ANOGA	Q7q737	anopheles g
34	120	2.7	1242	2	Q4X2J9_PLACH	Q4x2j9	plasmodium
35	120	2.7	1516	2	Q504M1_XENTR	Q504m1	xenopus tro
36	119	2.7	847	2	Q82J97_STRAW	Q82j97	streptomyce
37	118.5	2.7	774	2	Q9VAA2_DROME	Q9vaa2	drosophila
38	118.5	2.7	1688	2	Q68DY2_HUMAN	Q68dy2	homo sapien
39	118.5	2.7	2747	2	Q5GQW9_9CAUD	Q5gqw9	bacteriopha
40	118	2.7	1052	2	Q17657_CAEEL	Q17657	caenorhabdi
41	118	2.7	1700	2	Q8IWC7_HUMAN	Q8iwc7	homo sapien
42	118	2.7	2122	2	Q54R92_DICDI	Q54r92	dictyosteli
43	118	2.7	3494	2	Q7LC53_HUMAN	Q7lc53	homo sapien
44	118	2.7	5193	2	Q2QI47_MOUSE	Q2qi47	mus musculu
45	117.5	2.7	1464	2	Q23995_DROME	Q23995	drosophila

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